

SEQUENCE LISTING

<110> LIN, LEU-FEN H

COLLINS, FRANKLIN D

DOHERTY, DANIEL H

LILE, JACK

BEKTESH, SUSAN

<120> Glial Cell Line-Derived Neurotrophic Factor

<130> S-225E Rev

<140> 08/182,183

<141> 1994-05-23

<150> 07/764,685

<151> 1991-09-20

<150> 07/774,109

<151> 1991-10-08

<150> 07/788,423

<151> 1991-11-06

<150> 07/855,413

<151> 1992-03-19

<150> PCT/US92/07888

<151> 1992-09-17

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 25

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa in position 16 may be any one of the 20 naturally occurring amino acids.

<220>

<221> MISC_FEATURE

<223> N-terminal fragment

<400> 1

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Xaa
1 5 10 15

Gln Ala Ala Ala Ala Ser Pro Asp Asn
20 25

<210> 2

<211> 13

<212> PRT

<213> Rattus rattus

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<222> (2)..(2)

<223> Xaa in position 2 is either Lys or Gln

<220>

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<223> Internal GDNF peptide fragment

<400> 2

Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu
1 5 10

<210> 3

<211> 900

<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (25)..(705)

<223>

<220>

<221> mat_peptide

<222> (304)..()

<223>

<400> 3

cccccgggct gcaggaattc gggg gtc tac gga gac cgg atc cga ggt gcc 51
 Val Tyr Gly Asp Arg Ile Arg Gly Ala
 -90 -85

gcc gcc gga cgg gac tct aag atg aag tta tgg gat gtc gtg gct gtc 99
 Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val Ala Val
 -80 -75 -70

tgc ctg gtg ttg ctg cac acc gcg tct gcc ttc ccg ctg ccc gcc ggt 147
 Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly
 -65 -60 -55

aag agg ctt ctc gaa gcg ccc gcc gaa gac cac tcc ctc ggc cac cgc 195
 Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser Leu Gly His Arg
 -50 -45 -40

cgc gtg ccc ttc gcg ctg acc agt gac tcc aat atg ccc gaa gat tat 243
 Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn Met Pro Glu Asp Tyr
 -35 -30 -25

cct gac cag ttt gat gac gtc atg gat ttt att caa gcc acc atc aaa 291
 Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys
 -20 -15 -10 -5

aga ctg aaa agg tca cca gat aaa caa gcg gcg gca ctt cct cga aga 339
 Arg Leu Lys Arg Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg
 -1 1 5 10

gag agg aac cgg caa gct gca gct gcc agc cca gag aat tcc aga ggg 387
 Glu Arg Asn Arg Gln Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly
 15 20 25

aaa ggt cgc aga ggc cag agg ggc aaa aat cgg ggg tgc gtc tta act 435
 Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr
 30 35 40

gca ata cac tta aat gtc act gac ttg ggt ttg ggc tac gaa acc aag 483
 Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys
 45 50 55 60

gag gaa ctg atc ttt cga tat tgt agc ggt tcc tgt gaa gcg gcc gag 531
 Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu
 65 70 75

aca atg tac gac aaa ata cta aaa aat ctg tct cga agt aga agg cta 579
 Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu
 80 85 90

aca agt gac aag gta ggc cag gca tgt tgc agg ccg gtc gcc ttc gag 627
 Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp
 95 100 105

gac gac ctg tcg ttt tta gac gac agc ctg gtt tac cat atc cta aga 675
 Asp Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg
 110 115 120

aag cat tcc gct aaa cgg tgt gga tgt atc tgaccctggc tccagagact 725
 Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 125 130

gctgtgtatt gcattcctgc tacactgcga agaaagggac caagggtccc aggaaatatt 785

tgcccagaaa ggaagataag gaccaagaag gcagaggcag aggcggaaga agaagaagaa 845

aagaaggacg aaggcagcca tctgtgggag cctgtagaag gaggccacgc tacag 900

<210> 4

<211> 227

<212> PRT

<213> Rattus rattus

<400> 4

Val Tyr Gly Asp Arg Ile Arg Gly Ala Ala Ala Gly Arg Asp Ser Lys
 -90 -85 -80

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
 -75 -70 -65

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro
 -60 -55 -50

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr
 -45 -40 -35 -30

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
 -25 -20 -15

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
 -10 -5 -1 1

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
 5 10 15

Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
 20 25 30 35

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
 40 45 50

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
55 60 65

Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu
70 75 80

Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln
85 90 95

Ala-Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
100 105 110 115

Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
120 125 130

Gly Cys Ile

<210> 5

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24)..(506)

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<221> mat_peptide

<222> (105)..()

<223>

<400> 5

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Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln
-25 -20

ttc gat gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa 101
Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys
-15 -10 -5

agg tca cca gat aaa caa atg gca gtg ctt cct aga aga gag cgg aat 149
Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn
-1 1 5 10 15

cgg cag gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg 197
Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg
20 25 30

aga ggc cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat 245
 Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His
 35 40 45
 tta aat gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg 293
 Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
 50 55 60
 att ttt agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac 341
 Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
 65 70 75
 gac aaa ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac 389
 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp
 80 85 90 95
 aaa gta ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg 437
 Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
 100 105 110
 tcg ttt tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc 485
 Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
 115 120 125
 gct aaa agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt 536
 Ala Lys Arg Cys Gly Cys Ile
 130
 gcattcctgc tacagtgcaa agaaag 562

<210> 6

<211> 161

<212> PRT

<213> Homo sapiens

<400> 6

Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp
 -25 -20 -15
 Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln
 -10 -5 -1 1 5
 Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala
 10 15 20
 Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys
 25 30 35
 Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu
 40 45 50
 Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser
 55 60 65
 Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn
 70 75 80 85
 Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys

	90		95		100
Cys	Arg	Pro	Ile	Ala	Phe
	105		110		115
Leu	Val	Tyr	His	Ile	Leu
	120		125		130

Ile

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide probe

<220>

<221> misc_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (15)..(15)

<223> N at position 15 is inosine

<220>

<221> misc_feature

<222> (18)..(18)

<223> N at position 18 is inosine

<400> 7

ccngayaarc argcngcngc

20

<210> 8

<211> 223

<212> DNA

<213> Homo sapiens

<400> 8
ttctctcccc cacctccccg cgtccccg cgc aggtgccgcc gccggacggg actttaagat 60
gaagttatgg gatgtcgtgg ctgtctgcct ggtgctgctc cacaccgct cgccttccc 120
gctgcccgcc ggtaagaggg ctccccaggg gcccgccgaa gaccgctccc tcggccgccc 180
ccgcgcgccc ttcgcgctga gcagtgactg taagaaccgt tcc 223

<210> 9

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 9
cccgaattcg gg 12

<210> 10

<211> 7

<212> PRT

<213> Rattus rattus

<400> 10

Pro Asp Lys Gln Ala Ala Ala
1 5

<210> 11

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence from pBluescript SK-76.1 encoding rat GDNF
N-terminus sequence

<400> 11
gagaggaacc ggcaagctgc wgmwgywmwgm ccw 33

<210> 12

<211> 11

<212> PRT

<213> Rattus rattus

<400> 12

Glu Arg Asn Arg Gln Ala Ala Ala Ala Ser Pro
1 5 10

<210> 13

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide PCR primer DHD-26 to amplify DNA encoding rat GDNF polypeptide

<220>

<221> misc_feature

<222> (9)..(9)

<223> N at position 9 is inosine

<220>

<221> misc_feature

<222> (12)..(12)

<223> N at position 12 is inosine

<400> 13

arrttytna rnatytrtc

20

<210> 14

<211> 7

<212> PRT

<213> Rattus rattus

<220>

<221> misc_feature

<223> Internal rat GDNF peptide

<400> 14

Asp Lys Ile Leu Lys Asn Leu
1 5

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 15
gacgggactc taagatg

17

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer DHD23 to amplify rat GDNF probe

<220>

<221> misc_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (6)..(6)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (18)..(18)

<223> N at position 3 is inosine

<400> 16
gcngcngcyt gyttrtcngg

20

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LF2 to amplify rat GDNF probe

<400> 17
cgagacaatg tacgaca

17

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD2 to amplify rat GDNF probe

<400> 18
ctctggagcc aggggtca

17

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 19
cccgaattcg acgggactct aagatg

26

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LFA to amplify rat GDNF probe

<400> 20
cggtggccag agggagtggc cttc

24

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD3 to amplify human cDNA

<400> 21
cgcggtacca ataaggagga aaaaaaatgt caccagataa acaaat

46

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD4 to amplify human cDNA

<400> 22
cgcggtaccc agtctctgga gccgga

26

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic adapter fragment for plasmid pCJ1

<400> 23
gatctagaat tgtcatgttt gacagcttat cat

33

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Polylinker sequence for plasmid pCJX1-1 with EcoRI and PSTI overhangs

<400> 24
aattcccggt taccagatct gagctcacta gtctgca

37

<210> 25

<211> 747

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (32)..(691)

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<221> mat_peptide

<222> (290)..()

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-85 -80

ttt aag atg aag tta tgg gat gtc gtg gct gtc tgc ctg gtg ctg ctc 100
Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu
-75 -70 -65

cac acc gcg tcc gcc ttc ccg ctg ccc gcc ggt aag agg cct ccc gag 148
His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu
-60 -55 -50

gcg ccc gcc gaa gac cgc tcc ctc gcc cgc cgc cgc gcg ccc ttc gcg 196
Ala Pro Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala
-45 -40 -35

ctg agc agt gac tca aat atg cca gag gat tat cct gat cag ttc gat 244
Leu Ser Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp
-30 -25 -20

gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa agg tca 292
Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser

-15					-10					-5				-1	1	
cca gat aaa caa atg gca gtg ctt cct aga aga gag cgg aat cgg cag	340															
Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln																
5 10 15																
gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg aga ggc	388															
Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly																
20 25 30																
cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat tta aat	436															
Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn																
35 40 45																
gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg att ttt	484															
Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe																
50 55 60 65																
agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac gac aaa	532															
Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys																
70 75 80																
ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac aaa gta	580															
Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val																
85 90 95																
ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg tcg ttt	628															
Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe																
100 105 110																
tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc gct aaa	676															
Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys																
115 120 125																
agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt gcattcctgc	731															
Arg Cys Gly Cys Ile																
130																
tacagtgcaa agaaag	747															

<210> 26

<211> 220

<212> PRT

<213> Homo sapiens

<400> 26

Gly Ala Ala Ala Gly Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val
-85 -80 -75

Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro
-70 -65 -60 -55

Ala Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu Gly
-50 -45 -40

Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn Met Pro Glu
-35 -30 -25

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Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr
  -20          -15          -10

Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro
  -5          -1  1          5          10

Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser
      15          20          25

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val
      30          35          40
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Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu
      45          50          55

Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala
      60          65          70

Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg
      75          80          85          90

Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala
      95          100          105

Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile
      110          115          120

Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
      125          130

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<210> 27

<211> 211

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<223> Rat pre-pro GDNF

<400> 27

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Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
  1          5          10          15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro
      20          25          30

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr
      35          40          45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
      50          55          60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
      65          70          75          80

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Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
 85 90 95
 Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
 100 105 110
 Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
 115 120 125
 Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
 130 135 140
 Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu
 145 150 155 160
 Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln
 165 170 175
 Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 180 185 190
 Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
 195 200 205
 Gly Cys Ile
 210

<210> 28

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Human pre-pro GDNF

<400> 28

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
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 Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
 20 25 30
 Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
 35 40 45
 Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
 50 55 60
 Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
 65 70 75 80
 Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
 85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210